

AMP2.txt
SEQUENCE LISTING

<110> Liu, Chuan-Fa
Feige, Ulrich
Cheetham, Janet C.

<120> Thrombopoietic Compounds

<130> 01017/36263

<140>

<141>

<150> 60/105,348

<151> 1998-10-23

<160> 46

<170> PatentIn Ver. 2.0

<210> 1

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 1

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10

<210> 2

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<223> Peptide is a subunit of a homodimer: Subunits in
the dimer are covalently bonded at each carboxy
terminus through peptide linkage with
NH2-CH2-CH2-CH2-CH2-CH2-CH(CONH2)-NH-CO-CH2-CH2-NH2

<400> 2

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10

<210> 3

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 3

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gtcttctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 120
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 180
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 240
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 300

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aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 360
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 420
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 480
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 540
tccgacggct ccttcttctt ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 600
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 660
agcctctccc tgtctccggg taaa 684

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<210> 4

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 4

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tgtacgcacc accacctgca ctccgtgctt ctgggactcc agttcaagtt gacctgcac 180
ctgccgcacc tccacgtatt acggttctgt ttcggcgccc tcctcgtcat gttgtcgtgc 240
atggcacacc agtcgcagga gtggcaggac gtggctcctga ccgacttacc gttcctcatg 300
ttcacgttcc agaggttgtt tcgggagggg cgggggtagc tcttttggtg gaggtttcgg 360
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ttcttgggtc agtcggactg gacggaccag tttccgaaga tagggtcgct gtagcggcac 480
ctcaccctct cgttaccctg cggcctcttg ttgatgttct ggtgcggagg gcacgacctg 540
aggctgccga ggaagaagga gatgtcgttc gagtggcacc tgttctcgtc caccgtcgtc 600
cccttgacga agagtacgag gcactacgta ctccgagacg tgttggtgat gtgcgtcttc 660
tcggagagggg acagaggccc attt 684

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<210> 5

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 5

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Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
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Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
          20           25           30

```

```

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
          35           40           45

```

```

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
          50           55           60

```

```

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
          65           70           75           80

```

```

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
          85           90           95

```

```

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
          100          105          110

```

```

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
          115          120          125

```

```

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
          130          135          140

```

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Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 145 150 155 160
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 165 170 175
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 180 185 190
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 195 200 205
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 210 215 220
 Ser Pro Gly Lys
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<210> 6
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 6
 Gly Gly Gly Lys Gly Gly Gly Gly
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<210> 7
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 7
 Gly Gly Gly Asn Gly Ser Gly Gly
 1 5

<210> 8
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 8
 Gly Gly Gly Cys Gly Gly Gly Gly
 1 5

<210> 9
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 9

Gly Pro Asn Gly
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<210> 10
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 10
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Pro
1 5 10 15

Asn Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
20 25 30

<210> 11
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<223> Cyclic peptide; Secondary structure is maintained
by disulfide bond between intramolecular Cys
residues at positions 9 and 31

<400> 11
Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala Gly Gly
1 5 10 15

Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu
20 25 30

Ala Ala Arg Ala
35

<210> 12
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 12
Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala Gly Gly
1 5 10 15

Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Arg Leu Gln Cys Leu
20 25 30

Ala Ala Arg Ala
35

<210> 13

<211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 13
 Ile Glu Gly Pro Thr Leu Arg Gln Ala Leu Ala Ala Arg Ala Gly Gly
 1 5 10 15
 Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Ala Leu
 20 25 30
 Ala Ala Arg Ala
 35

<210> 14
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 14
 Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
 1 5 10 15
 Gly Lys Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
 20 25 30
 Ala Ala Arg Ala
 35

<210> 15
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Lys residue at position 18 is Bromoacetylated

<220>
 <223> Description of Artificial Sequence: derivatized
 peptide

<400> 15
 Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
 1 5 10 15
 Gly Lys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
 20 25 30
 Ala Ala Arg Ala
 35

<210> 16
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

AMP2.txt

<400> 16
 Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
 1 5 10 15
 Gly Cys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
 20 25 30
 Ala Ala Arg Ala
 35

<210> 17
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Lys at position 18 is pegylated
 <220>
 <223> Description of Artificial Sequence: derivatized
 peptide

<400> 17
 Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
 1 5 10 15
 Gly Lys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
 20 25 30
 Ala Ala Arg Ala
 35

<210> 18
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cys at position 18 is pegylated
 <220>
 <223> Description of Artificial Sequence: derivatized
 peptide

<400> 18
 Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
 1 5 10 15
 Gly Cys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
 20 25 30
 Ala Ala Arg Ala
 35

<210> 19
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide
 <400> 19

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
 1 5 10 15
 Gly Asn Gly Ser Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
 20 25 30
 Ala Ala Arg Ala
 35

<210> 20
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Monomeric subunit of a homodimer; Subunits in the homodimer are bonded by a disulfide bond between Cys residues at position 18 on each subunit

<220>
 <223> Description of Artificial Sequence: peptide

<400> 20
 Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
 1 5 10 15
 Gly Cys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
 20 25 30
 Ala Ala Arg Ala
 35

<210> 21
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 21
 Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
 1 5 10 15
 Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
 20 25 30
 Ala Ala Arg Ala
 35

<210> 22
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide is derivatized at the amino terminus with a covalently bonded immunoglobulin Fc region

<220>
 <223> Description of Artificial Sequence: peptide

<400> 22
 Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Pro

1

5

15

Asn Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
20 25 30

<210> 23

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide is covalently bonded at the amino and
carboxy termini to an immunoglobulin Fc region

<220>

<223> Description of Artificial Sequence: peptide

<400> 23

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Pro
1 5 10 15

Asn Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
20 25 30

<210> 24

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide is copvalently bonded at the carboxy
terminus to an immunoglobulin Fc region

<220>

<223> Description of Artificial Sequence: peptide

<400> 24

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
1 5 10 15

Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
20 25 30

Ala Ala Arg Ala
35

<210> 25

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide is covalently bonded at the amino terminus
to an immunoglobulin Fc region

<220>

<223> Description of Artificial Sequence: peptide

AMP2.txt

<400> 25
Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Gly Pro Asn Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala
20 25 30

Arg Ala

<210> 26

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide is covalently bonded at the amino terminus
to an immunoglobulin Fc region

<220>

<223> Description of Artificial Sequence: peptide

<400> 26

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
1 5 10 15

Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
20 25 30

Ala Ala Arg Ala
35

<210> 27

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide is covalently bonded at the amino terminus
to an immunoglobulin Fc region

<220>

<223> Cyclic peptide; Secondary structure is maintained
by disulfide linkage between intramolecular Cys
residues at positions 9 and 31

<220>

<223> Description of Artificial Sequence: peptide

<400> 27

Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala Gly Gly
1 5 10 15

Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu
20 25 30

Ala Ala Arg Ala
35

<210> 28

<211> 36

<212> PRT

<213> Artificial Sequence

AMP2.txt

<220>
<223> Peptide is covalently bonded at the amino terminus
to an immunoglobulin Fc region

<220>
<223> Description of Artificial Sequence: peptide

<400> 28
Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala Gly Gly
1 5 10 15
Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu
20 25 30
Ala Ala Arg Ala
35

<210> 29
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<223> Peptide is covalently bonded at the amino terminus
to an immunoglobulin Fc region

<400> 29
Ile Glu Gly Pro Thr Leu Arg Gln Ala Leu Ala Ala Arg Ala Gly Gly
1 5 10 15
Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Ala Leu
20 25 30
Ala Ala Arg Ala
35

<210> 30
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide is covalently bonded at the amino terminus
to an immunoglobulin Fc region

<220>
<223> Description of Artificial Sequence: peptide

<400> 30
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
1 5 10 15
Gly Lys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
20 25 30
Ala Ala Arg Ala
35

<210> 31
<211> 36
<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide is covalently bonded at the amino terminus to an immunoglobulin Fc region

<220>

<223> Description of Artificial Sequence: peptide

<400> 31

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
1 5 10 15

Gly Cys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
20 25 30

Ala Ala Arg Ala
35

<210> 32

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<223> Peptide is covalently bonded at the amino terminus to an immunoglobulin Fc region

<400> 32

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
1 5 10 15

Gly Asn Gly Ser Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
20 25 30

Ala Ala Arg Ala
35

<210> 33

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<223> Peptide is a subunit of a homodimer; subunits in the homodimer are covalently bonded through a disulfide bond between Cys residues at position 18 of each subunit

<220>

<223> Peptide is covalently bonded at the amino terminus to an immunoglobulin Fc region

<400> 33

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly
1 5 10 15

Gly Cys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
20 25 30

AMP2.txt

Ala Ala Arg Ala
35

<210> 34
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<223> Peptide is covalently bonded at the amino terminus
to an immunoglobulin Fc region

<400> 34
Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala
1 5 10 15

Ala Arg Ala Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr
20 25 30

Leu Arg Gln Trp Leu Ala Ala Arg Ala
35 40

<210> 35
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 35
aaagggtggag gtggtggtat cgaagggtccg actctgcgctc agtggctggc tgctcgtgct 60

<210> 36
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 36
acctccacca ccagcacgag cagccagcca ctgacgcaga gtcggacc 48

<210> 37
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 37
ggtggtggag gtggcgggcg aggtattgag ggcccaaccc ttcgccaatg gcttgcagca 60
cgcgca 66

<210> 38
<211> 76

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 38
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caatacctcc gccgcc 76

<210> 39
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 39
aaagggtggag gtggtggtat cgaagggtccg actctgcgtc agtggctggc tgctcgtgct 60
ggtggtggag gtggcggcgg aggtattgag ggcccaaccc ttcgccaatg gcttgagca 120
cgcgca 126

<210> 40
<211> 124
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 40
ccaggctgag acgcagtcac cgaccgacga gcacgaccac cacctccacc gccgcctcca 60
taactcccgg gttgggaagc ggttaccgaa cgctcgtgcgc gtattagagc tcctaggaaa 120
aaaa 124

<210> 41
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 41
Lys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu
1 5 10 15
Ala Ala Arg Ala Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro
20 25 30
Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
35 40

<210> 42
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

AMP2.txt

<400> 42
aacataagta cctgtaggat cg 22

<210> 43
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 43
ttcgatacca ccacctccac ctttaccgag agacagggag aggctcttct gc 52

<210> 44
<211> 861
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 44
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caccttgtcc agctccggaa ctctctcttc ccccaaaaac 120
ccaaggacac cctcatgac tcccggaccc ctgaggtcac atgcgtgggtg gtggacgtga 180
gccacgaaga cctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 240
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc agcgtcctca 300
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ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc cgagaaccac 420
agggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccagggtc agcctgacct 480
gcctgggtcaa aggccttctat cccagcgaca tcgccgtgga gtgggagagc aatgggcagc 540
cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc ttcttctctt 600
acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg 660
tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg tctccgggta 720
aaggtggagg tgggtggtac gaaggtccga ctctgcgtca gtggctgggt gctcgtgctg 780
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gcgcataatc tcgaggatcc g 861

<210> 45
<211> 861
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 45
agatctaaac aaaattgatt aatttcctcc ttattgtata cctgttttga gtgtgtacag 60
gtggaacagg tcgaggcctt gaggaacccc ctggcagtca gaaggagaag ggggggtttt 120
ggttcctgtg ggagtactag agggcctggg gactccagtg tacgcaccac cacctgcact 180
cggtgtctct gggactccag ttcaagtga ccattgcacct gccgcacctc cacgtattac 240
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gggaggggtg ggggtagctc ttttggtaga ggttcgggt tcccgtcggg gctcttggtg 420
ttcacatgtg ggacgggggt agggccctac tcgactggtt cttgggtccag tcggactgga 480
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gcctcttggt gatgttctgg tgcggagggc acgacctgag gctgccgagg aagaaggaga 600
tgtcgttcca gtggcacctg ttctcgtcca cgcgtgctcc cttgcagaag agtacgaggc 660
actacgtact ccgagacgtg ttggtgatgt gcgtcttctc ggagagggac agaggcccat 720
ttccacctcc accaccatag ctccaggct gagacgcagt caccgaccga cgagcacgac 780
caccacctcc accgccgcct ccataactcc cgggttgagg agcggttacc gaacgtcgtg 840
cgcgattagg agctcctagg c 861

AMP2.txt

<210> 46
 <211> 269
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 46
 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 1 5 10 15
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 20 25 30
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 35 40 45
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 50 55 60
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 65 70 75 80
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 85 90 95
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 100 105 110
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 115 120 125
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 130 135 140
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 145 150 155 160
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 165 170 175
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 180 185 190
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 195 200 205
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 210 215 220
 Ser Pro Gly Lys Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg
 225 230 235 240
 Gln Trp Leu Ala Ala Arg Ala Gly Gly Gly Gly Gly Gly Gly Ile
 245 250 255
 Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
 260 265